

1
GTCTTCCACCATGCACTCGCTGGGCTTCTCTCTGTGGCGTGTCTCTCTGCTCGCCGCTG
-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGTGTGACGTAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGCGGAC
M H S L G F F S V A C S L L A A A
60

61
CGCTGCTCCCGGGTCTCGCGAGGCGCCGCCGCCGCCGCCCTTCGAGTCCGGACTCG
-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGGCCAGGAGCGCTCCGGGGCGGGCGGGCGGGAAGCTCAGGCCTGAGC
L L P G P R E A P A A A A A F E S G L D
120

121
ACCTCTCGGACGGGAGCCCCGACGGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG
-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGGAATACGTTCTGTCTAGACC
L S D A E P D A G E A T A Y A S K D L E
180

181
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT
-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y
240

241
ATTGGAAAATGTACAAGTGTCAAGTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCCCTTTCCTCCGACCGTTGTATTGTCTCTTGTC
W K M Y K C Q L R K G G W Q H N R E Q A
300

301
CCAACCTCAACTCAAGGACAGAAAGAGACTATAAAATTGCTGCAGCACATTATAACAG
-----+-----+-----+-----+-----+-----+-----+-----+
GGTGGAGTTGAGTTCCTGCTCTCTGATATTTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E
360

FIG. 1A

MATCH WITH FIG. 1B



MATCH WITH FIG. 1A

361 AGATCTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
-----+-----+-----+-----+-----+-----+-----+
TCTAGAACTTTTTCATAAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C
420

421 GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
-----+-----+-----+-----+-----+-----+-----+
CATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V
480

481 TGTCCGCTACAGATGTGGGGGTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
-----+-----+-----+-----+-----+-----+-----+
ACAGGCAGATGTCTACACCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
S V Y R C G G C C N S E G L Q C M N T S
540

541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCA
-----+-----+-----+-----+-----+-----+-----+
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGT
T S Y L S K T L F E I T V P L S Q G P K
600

601 AACCAGTAACAATCAGTTTGGCCAAATCACACTTCCTGCCGATGCATGCTAAACTGGATG
-----+-----+-----+-----+-----+-----+-----+
TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
P V T I S F A N H T S C R C M S K L D V
660



MATCH WITH FIG. 1B

661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
-----+-----+-----+-----+-----+
AAATGTCTGTTCAAGTAAGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG
Y R Q V H S I I R R S L P A T L P Q C Q
720

721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
-----+-----+-----+-----+-----+
TCCGTGCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
A A N K T C P T N Y M W N N H I C R C L
780

781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAATAACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D D S T D G F H
840

841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A
900

901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT
-----+-----+-----+-----+-----+
GCCCCGAAGCCGACGGTCGACACCTGGGGTGTCTTGTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C
960

MATCH WITH FIG. 1C

961	GTGTCGTAAAAAACAACCTCTTCCCCAGCCAATGTGGGGCCCAACCGAGAATTTGATGAAA -----+-----+-----+-----+-----+-----+-----+ CACAGACATTTTGTGAGAGGGGTTCGGTTACACCCCGGTGGCTCTTAAACACTACTTT V C K N K L F P S Q C G A N R E F D E N	1020
1021	ACACATGCCAGTGTGTATGTAAAAAGAACCTGCCCCAGAAAATCAACCCCTAAATCCTCGAA -----+-----+-----+-----+-----+-----+-----+ TGTGTACGGTCACACATACATTTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT T C Q C V C K R T C P R N Q P L N P G K	1080
1081	AATGTGCCCTGTGAATGTACAGAAAAGTCCACAGAAAATGCTTGTAAAAAGAAAGATTCC -----+-----+-----+-----+-----+-----+-----+ TTACACGGACACTTACATGTCCTTTCAGGTGCTTTACGAACAATTTCCCTTCTTCAAGG C A C E C T E S P Q K C L L K G K K F H	1140
1141	ACCACCAAACATGCAGCTGTTACAGACGGCCCATGTACGAACCCGACAGAGGCTTGTGAGC -----+-----+-----+-----+-----+-----+-----+ TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG H Q T C S C Y R R P C T N R Q K A C E P	1200
1201	CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTTGGCAAAGACCAC -----+-----+-----+-----+-----+-----+-----+ GTCCTAAAAGTATATCACTTCTTACACAGCAACACACAGGGAAGTATAACCGTTTCTGGTG G F S Y S E E V C R C V P S Y W Q R P Q	1260

FIG. 1D

MATCH WITH FIG. 1E



1674

FIG. 1E

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+-----+
61 AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAATAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
121 GAAAGGAGGCTGGCAACATAACAGAGAAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
-----+-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

MATCH WITH FIG. 2B

FIG. 2A

MATCH WITH FIG. 2A

421 TGA A A T T A C A G T G C C T C T C T C A A G G C C C C A A A C C A G T A C A A T C A G T T T G C C A A T C A
 E I T V P L S Q G P K P V T I S F A N H

481 C A C T T C C T G C C G A T G C A T G T T A A A C T G G A T G T T T A C A G A C A A G T T C A T T C C A T T A T T A G
 T S C R C M S K L D V Y R Q V H S I I R

541 A C G T T C C C T G C C A G C A A C A C T A C C A C A G T G T C A G G C A G C G A A C A A G A C C T G C C C C A C C A A
 R S L P A T L P Q C Q A A N K T C P T N

601 T T A C A T G T G G A A T A A T C A C A T C T G C A G A T G C C T G G C T C A G G A A G A T T T A T G T T T C C T C
 Y M W N N H I C R C L A Q E D F M F S S

661 G G A T G C T G G A G A T G A C T C A A C A G A T G G A T T C C A T G A C A T C T G T G G A C C A A A C A A G G A G C T
 D A G D D S T D G F H D I C G P N K E L

721 G G A T G A G A G A C C T G T C A G T G T G T C T G C A G A G C G G G G C T T C G G C C T G C C A G C T G T G G A C C
 D E E T C Q C V C R A G L R P A S C G P

MATCH WITH FIG. 2C

FIG. 2B



1141 GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
-----+-----+-----+-----+-----+-----+-----+
1201 GAGACCCCTGTGGGTCCATGCTAACAAAGACAAAAAGTCTGTCTTTTCCTGAACCATGTGGA
-----+-----+-----+-----+-----+-----+-----+
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAAGACTGGTTTT
-----+-----+-----+-----+-----+-----+-----+
1321 CTGCCAATGACCAACAGCCCAAGATTTCCCTCTTGTGATTTCTTTAAAAGAATGACTATA
-----+-----+-----+-----+-----+-----+-----+
1381 TAAATTTATTTCCCACTAAAAATATTGTTTCTGTCATTCATTTTATAGCAACAACAATTGGT
-----+-----+-----+-----+-----+-----+-----+
1441 AAAACTCACTGTGATCAATATTTTTTATATCATGCAAAAATATGTTTAAAAATAAAATGAAAA
-----+-----+-----+-----+-----+-----+-----+
1501 TTGTATTATAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

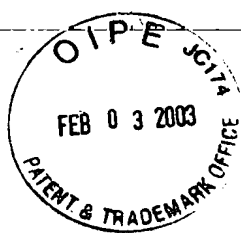
FIG. 2D

1		50
Pdgfa	.MRTLACLLL LCCYLALVL AEEAIPREV IERLARSOIH SIRDLORLLE	
Pdgfb	MNRCAW.LFL SLCCYLRLVS AEGDPIPEEL YEMLSOHSIR SFDDLORLLH	
VegfMNFL SWHWSLALL LY.....LHHAKWSOA	
Vegf2MTV LYPEYWKMYK CQ.....LRKGGWQHN	
51		100
Pdgfa	IDSVGSEDSL DLSLRAHGVH ATKHVPEKRP LPIRRKRSI.....EEAVP	
Pdgfb	GDP.GEEDGA ELDLNMTRSH SGGELES...LARGRRSLG SLTIAEPAMI	
Vegf	APMAE.....GGCQ NHHEVVKFMD.VYQR.....	
Vegf2	REQANLSRT EETIKFAAH YNTEILKSID NEWRK.....	
101		150
Pdgfa	AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCCTGCC NTSSVKQOPS	
Pdgfb	AECKTRTEVF EISRRLLDRT NANFLWPPC VEVQRCSCCC NNRNVQCRPT	
Vegf	SYCHPIETLV DIFQEYPDEI..EYIFKPS VPLMRGCGCC NDEGLECVPT	
Vegf2	TQCMPREVCI DVGKEFGVAT..NTFFKPPC VSVYRCGCGCC NSEGLQGMNT	
151		200
Pdgfa	RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEQAC.....AT.....	
Pdgfb	QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACQ.....ETVAAARPVT	
Vegf	EESNITMQIM RIK.PH..QC QHIGEMSFLO HNKCELRPKK DRAROEKKS	
Vegf2	STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSQDMSKL DVYROVHSII	

FIG. 3A

201		250
PdgfaTSLNPD YREEDTDVR.	
Pdgfb	RSPGGSQEQR AKTPQTRVTI	RTVVRVRPPK GKHKFKHHTH DKTALKE TLG
Vegf	RCK.....CKGQKRKRK	KSRYSWSVY VGARCCCLMPW SLPQPHHP
Vegf2	RRSLPATLPQ COAANKTCPT	NYMNNHICR CLAQEDFMFS SDAGDDSDTG
251		300
Pdgfa	
Pdgfb	A.....	
VegfCCP.....	CSE RRKHLFVQDP QTKCSCSKNT
Vegf2	FHDICGNKE LDEETCCQVC	RAGLRPASCG PHKEL...DR NSCQCVCCKNK
301		350
Pdgfa	
Pdgfb	
Vegf	DSRCKARQ LELNERTCRC DKPRR	
Vegf2	LFPSQCCANR EFDENTCQC	VCKRTCPRNQ PLNPGKCACE CTESPOKCLL
351		398
Pdgfa	
Pdgfb	
Vegf	
Vegf2	KGKKFHHQTC SCYRRPCTNR	QKACEPGFSY SEEVCRCPVS YWQRPQMS

FIG. 3B

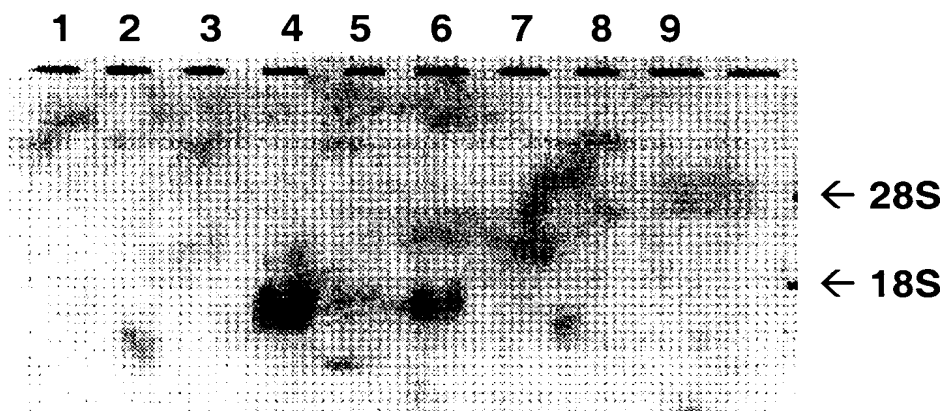


PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN
EACH PAIR OF GENES IS SHOWN IN THE
FOLLOWING TABLE

	PDGF α	PDGF β	VEGF	VEGF-2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF-2	28.5	22.4	30.0	

FIG. 4

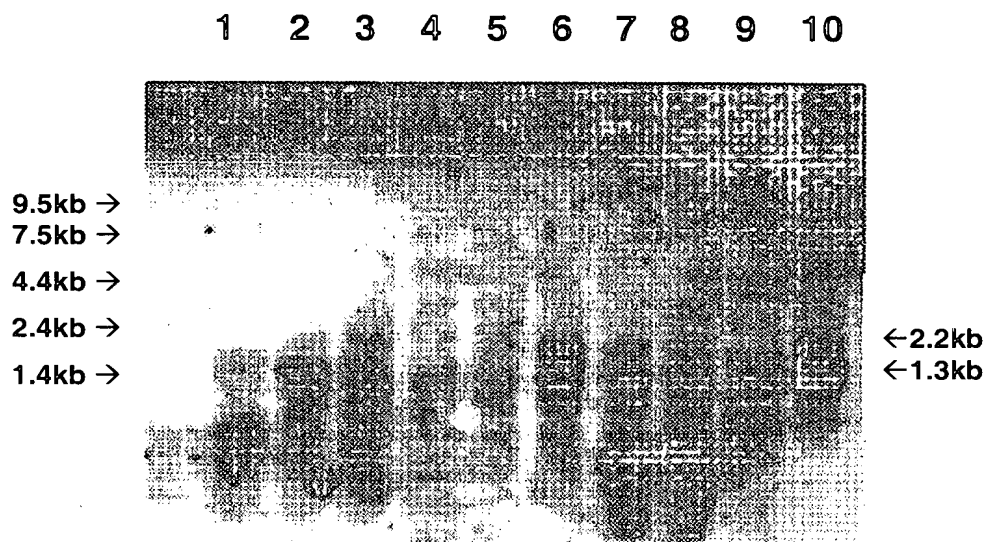
Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1	Normal Tissue
Lane 2	Breast Tumor Tissue
Lanes 3-9	Breast Tumor Cell Lines

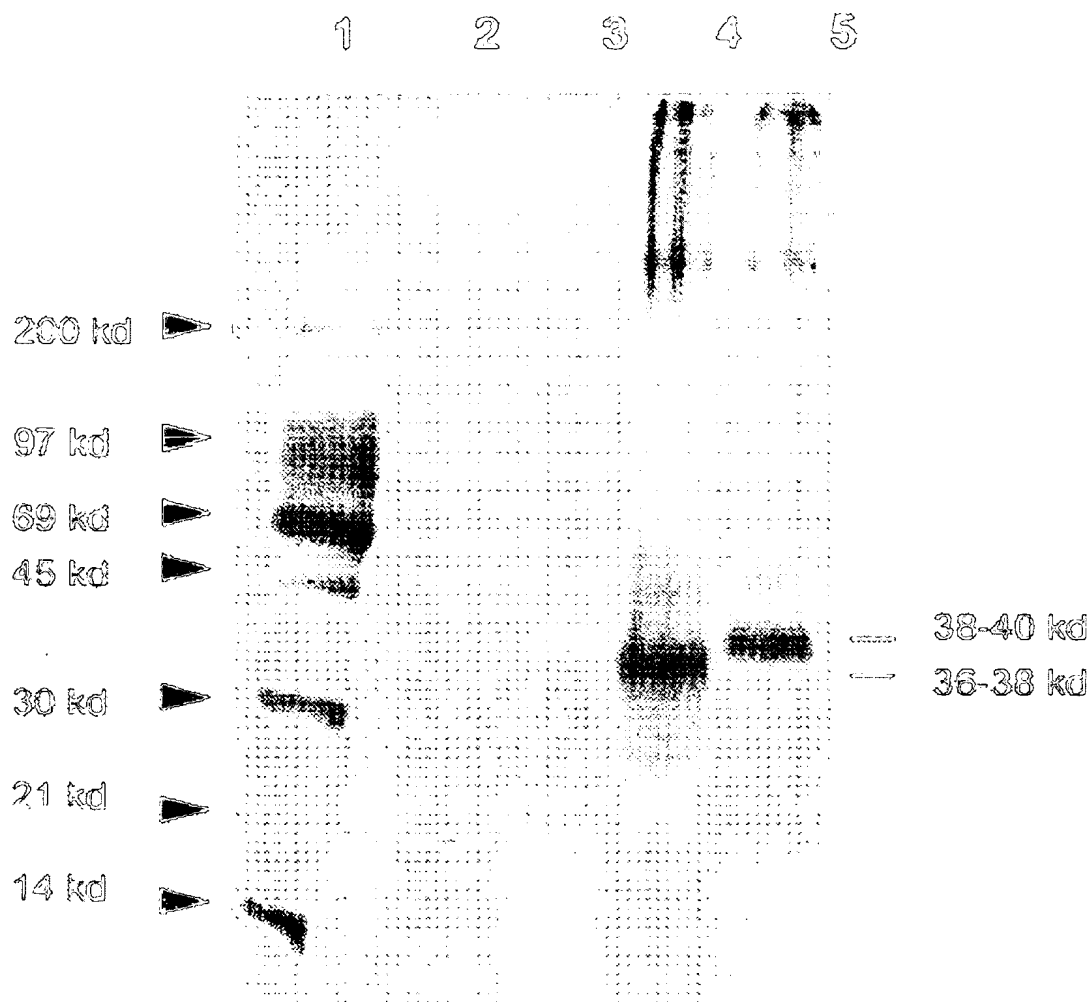
FIG. 5

Expression of VEGF2 mRNA in Human Adult Tissues



- | | |
|----------------|----------------|
| 1. Ovary | 6. Lung |
| 2. Testes | 7. Spleen |
| 3. Gall Blader | 8. Prostate |
| 4. Kidney | 9. Hippocampus |
| 5. Liver | 10. Heart |

FIG. 6



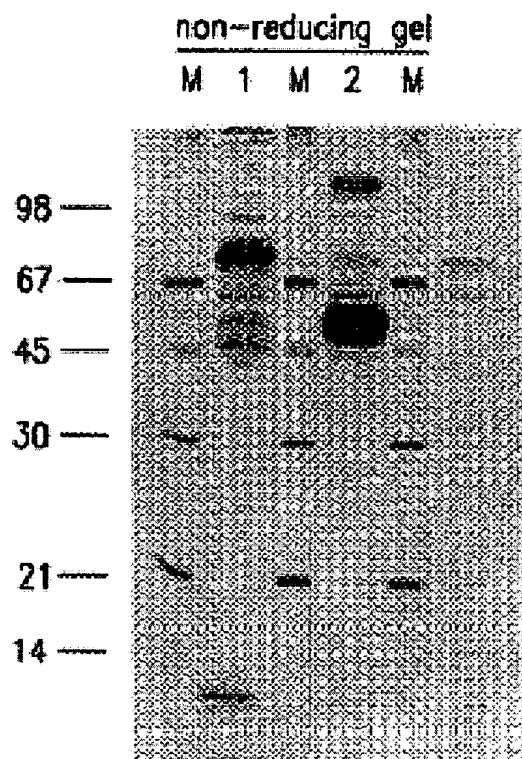
- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primer)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primer)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primer)

FIG. 7



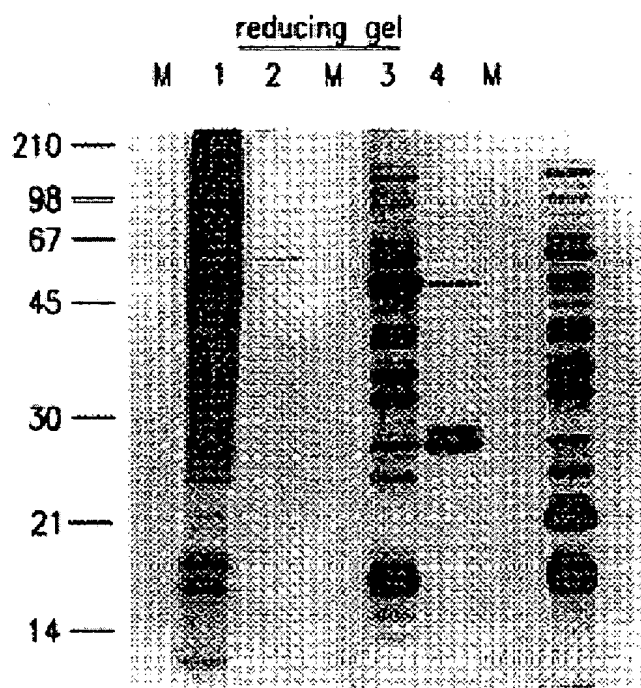
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Lane M: Marker
Lane 1: Vector medium
Lane 2: VEGF2 medium

FIG. 8A



Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

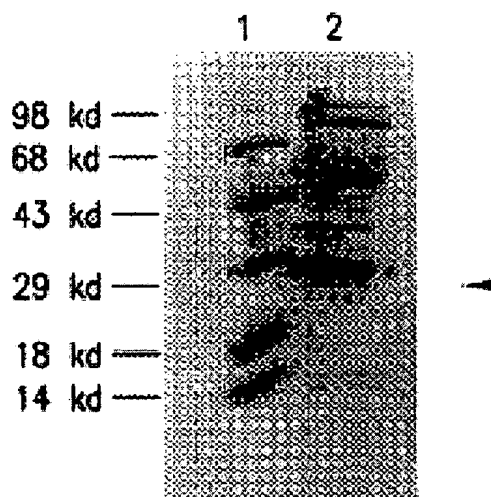


FIG. 9

Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

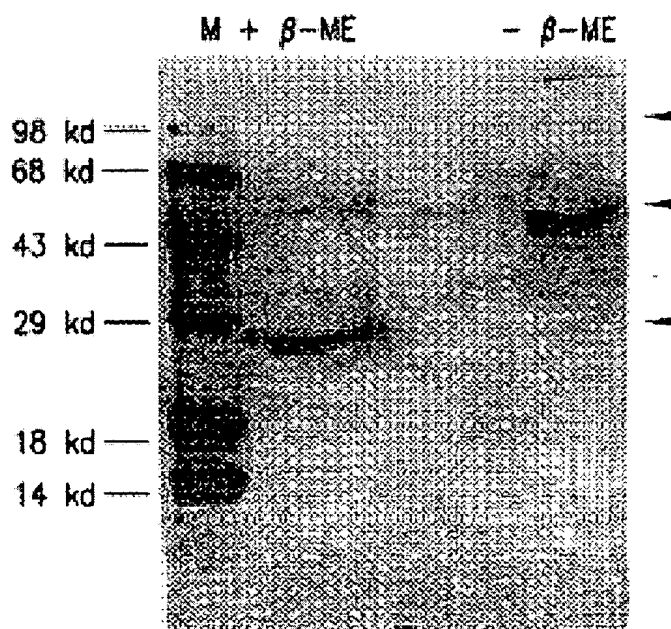


FIG. 10



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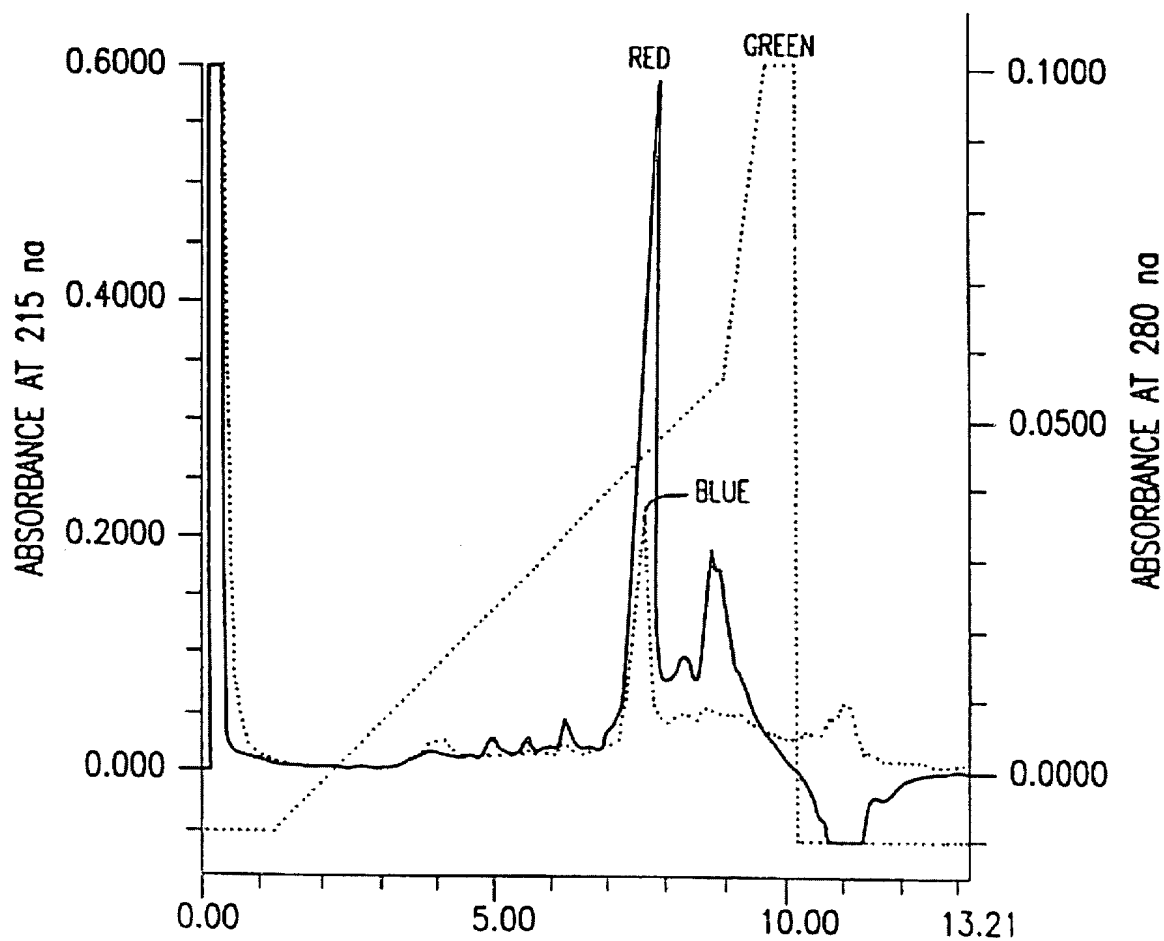


FIG. 11

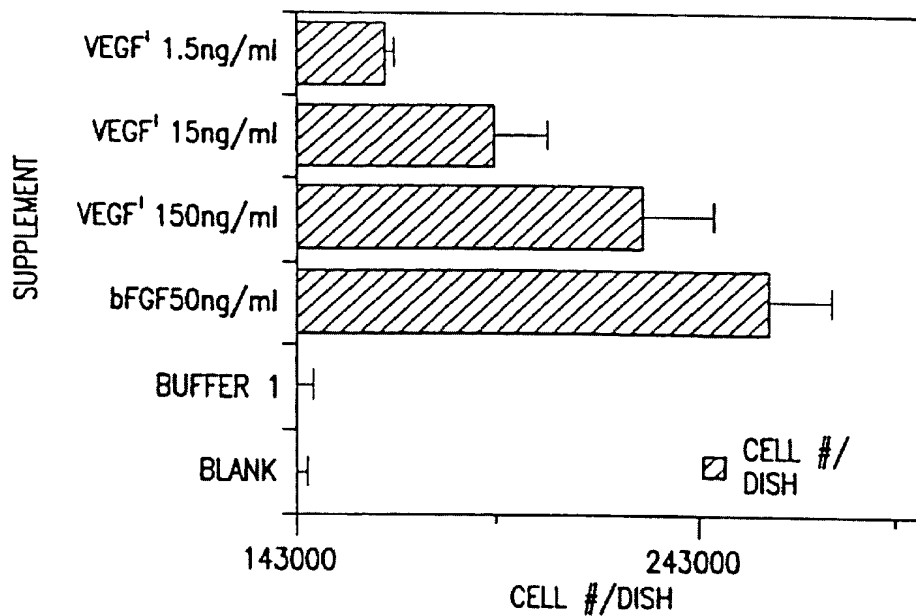


FIG. 12

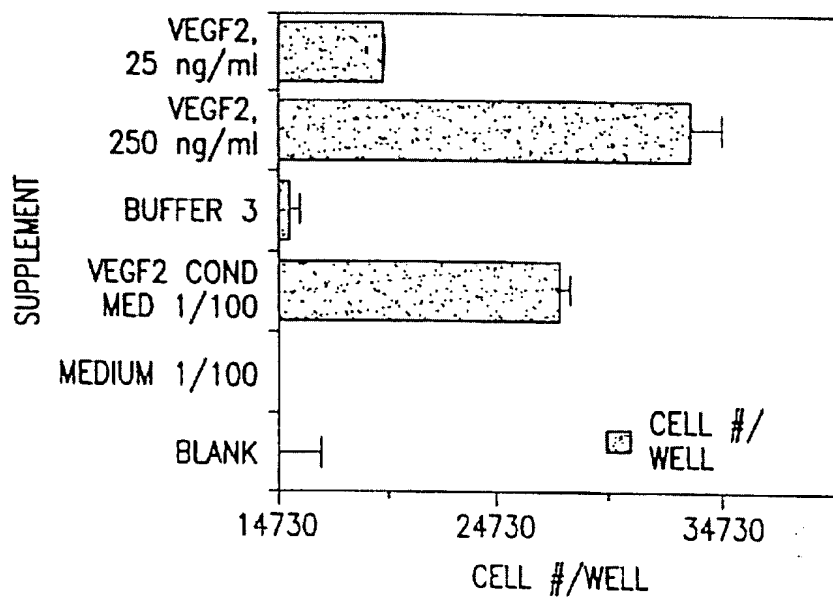


FIG. 13